

SEQUENCE LISTING

<110> Haldeman, Betty A.
Thayer, Edward C.
Sheppard, Paul O.

<120> ADIPOCYTE COMPLEMENT RELATED PROTEIN
ZACRP3X2

<130> 00-111D1

<150> US 10/012,605

<151> 2001-12-07

<150> US 60/254,019

<151> 2000-12-07

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 957

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(957)

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1 5 10 15	
ctc cct ttt tgc ctg tgt caa gat gaa tac atg gag gtg agc gga aga	96
Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Val Ser Gly Arg	
20 25 30	
act aat aaa gtg gtg gca aga ata gtg caa agc cac cag cag act ggc	144
Thr Asn Lys Val Val Ala Arg Ile Val Gln Ser His Gln Gln Thr Gly	
35 40 45	
cgt agc ggc tcc agg agg gag aaa gtg aga gag cgg agc cat cct aaa	192
Arg Ser Gly Ser Arg Arg Glu Lys Val Arg Glu Arg Ser His Pro Lys	
50 55 60	
act ggg act gtg gat aat aac act tct aca gac cta aaa tcc ctg aga	240
Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp Leu Lys Ser Leu Arg	
65 70 75 80	
cca gat gag cta ccg cac ccc gag gta gat gac cta gcc cag atc acc	288
Pro Asp Glu Leu Pro His Pro Glu Val Asp Asp Leu Ala Gln Ile Thr	
85 90 95	
aca ttc tgg ggc cag tct cca caa acc gga gga cta ccc cca gac tgc	336
Thr Phe Trp Gly Gln Ser Pro Gln Thr Gly Gly Leu Pro Pro Asp Cys	
100 105 110	
agt aag tgt tgt cat gga gac tac agc ttt cga ggc tac caa ggc ccc	384
Ser Lys Cys Cys His Gly Asp Tyr Ser Phe Arg Gly Tyr Gln Gly Pro	
115 120 125	
cct ggg cca ccg ggc cct cct ggc att cca gga aac cat gga aac aat	432
Pro Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Asn His Gly Asn Asn	
130 135 140	

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ggc aac aat gga gcc act ggt cat gaa gga gcc aaa ggt gag aag ggc 480
Gly Asn Asn Gly Ala Thr Gly His Glu Gly Ala Lys Gly Glu Lys Gly 160
145                               150                               155

gac aaa ggt gac ctg ggg cct cga ggg gag cgg ggg cag cat ggc ccc 528
Asp Lys Gly Asp Leu Gly Pro Arg Gly Glu Arg Gly Gln His Gly Pro 175
                               165                               170                               175

aaa gga gag aag ggc tac ccg ggg att cca cca gaa ctt cag att gca 576
Lys Gly Glu Lys Gly Tyr Pro Gly Ile Pro Pro Glu Leu Gln Ile Ala 190
                               180                               185                               190

ttc atg gct tct ctg gca acc cac ttc agc aat cag aac agt ggg att 624
Phe Met Ala Ser Leu Ala Thr His Phe Ser Asn Gln Asn Ser Gly Ile 205
                               195                               200                               205

atc ttc agc agt gtt gag acc aac att gga aac ttc ttt gat gtc atg 672
Ile Phe Ser Ser Val Glu Thr Asn Ile Gly Asn Phe Phe Asp Val Met 220
                               210                               215                               220

act ggt aga ttt ggg gcc cca gta tca ggt gtg tat ttc ttc acc ttc 720
Thr Gly Arg Phe Gly Ala Pro Val Ser Gly Val Tyr Phe Phe Thr Phe 240
225                               230                               235                               240

agc atg atg aag cat gag gat gtt gag gaa gtg tat gtg tac ctt atg 768
Ser Met Met Lys His Glu Asp Val Glu Glu Val Tyr Val Tyr Leu Met 255
                               245                               250                               255

cac aat ggc aac aca gtc ttc agc atg tac agc tat gaa atg aag ggc 816
His Asn Gly Asn Thr Val Phe Ser Met Tyr Ser Tyr Glu Met Lys Gly 270
                               260                               265                               270

aaa tca gat aca tcc agc aat cat gct gtg ctg aag cta gcc aaa ggg 864
Lys Ser Asp Thr Ser Ser Asn His Ala Val Leu Lys Leu Ala Lys Gly 285
                               275                               280                               285

gat gag gtt tgg ctg cga atg ggc aat ggc gct ctc cat ggg gac cac 912
Asp Glu Val Trp Leu Arg Met Gly Asn Gly Ala Leu His Gly Asp His 300
290                               295                               300

caa cgc ttc tcc acc ttt gca gga ttc ctg ctc ttt gaa act aag 957
Gln Arg Phe Ser Thr Phe Ala Gly Phe Leu Leu Phe Glu Thr Lys 315
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<212> PRT
<213> Homo sapiens

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20      25      30
Thr Asn Lys Val Val Ala Arg Ile Val Gln Ser His Gln Thr Gly
35      40      45
Arg Ser Gly Ser Arg Arg Glu Lys Val Arg Glu Arg Ser His Pro Lys
50      55      60
Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp Leu Lys Ser Leu Arg
65      70      75      80
Pro Asp Glu Leu Pro His Pro Glu Val Asp Asp Leu Ala Gln Ile Thr
85      90      95
Thr Phe Trp Gly Gln Ser Pro Gln Thr Gly Gly Leu Pro Pro Asp Cys

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95          100          105          110
ggg att cca cca gaa ctt cag att gca ttc atg gct tct ctg gca acc 446
Gly Ile Pro Pro Glu Leu Gln Ile Ala Phe Met Ala Ser Leu Ala Thr
115          120          125

cac ttc agc aat cag aac agt ggg att atc ttc agc agt gtt gag acc 494
His Phe Ser Asn Gln Asn Ser Gly Ile Phe Ser Ser Val Glu Thr
130          135          140

aac att gga aac ttc ttt gat gtc atg act ggt aga ttt ggg gcc cca 542
Asn Ile Gly Asn Phe Phe Asp Val Met Thr Gly Arg Phe Gly Ala Pro
145          150          155

gta tca ggt gtg tat ttc ttc acc ttc agc atg atg aag cat gag gat 590
Val Ser Gly Val Tyr Phe Phe Thr Phe Ser Met Met Lys His Glu Asp
160          165          170

gtt gag gaa gtg tat gtg tac ctt atg cac aat ggc aac aca gtc ttc 638
Val Glu Glu Val Tyr Val Tyr Leu Met His Asn Gly Asn Thr Val Phe
175          180          185          190

agc atg tac agc tat gaa atg aag ggc aaa tca gat aca tcc agc aat 686
Ser Met Tyr Ser Tyr Glu Met Lys Gly Lys Ser Asp Thr Ser Ser Asn
195          200          205

cat gct gtg ctg aag cta gcc aaa ggg gat gag gtt tgg ctg cga atg 734
His Ala Val Leu Lys Leu Ala Lys Gly Asp Glu Val Trp Leu Arg Met
210          215          220

ggc aat ggc gct ctc cat ggg gac cac caa cgc ttc tcc acc ttt gca 782
Gly Asn Gly Ala Leu His Gly Asp His Gln Arg Phe Ser Thr Phe Ala
225          230          235

gga ttc ctg ctc ttt gaa act aag taaatatatg actagaatag ctccactttg 836
Gly Phe Leu Leu Phe Glu Thr Lys
240          245

gggaagactt gtagctgagc tgatttggtta cgatctgagg aacattaaag ttgagggttt 896
tacattgctg tattcaaaaa attattgggtt gcaatgttgt tcacgctaca ggtacaccaa 956
taatgttgga caattcaggg gctcagaaga atcaaccaca aaatagtctt ctcagatgac 1016
cttgactaat atactcagca tctttatcac tctttccttg gcacctaaaa gataattctc 1076
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tccccacat cgcccccaac ttcggatgtg gggtcaggag gttgagggtc actattaaca 1496
aatgtcataa atatctcata gaggtacagt gccaatagat attcaaagt tgcattgtga 1556
ccagagggat tttatatctg aagaacatac actattaata aataccttag agaaagattt 1616
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1696

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<211> 219
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<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(219)

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Val Ser Gly Arg Thr Asn Lys Val Val Ala Arg Ile Val Gln Ser His

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cag cag act ggc cgt agc ggc tcc agg agg gag aaa gtg aga gag cgg	96			
Gln Gln Thr Gly Arg Ser Gly Ser Arg Arg Glu Lys Val Arg Glu Arg				
20 25 30				
agc cat cct aaa act ggg act gtg gat aat aac act tct aca gac cta	144			
Ser His Pro Lys Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp Leu				
35 40 45				
aaa tcc ctg aga cca gat gag cta ccg cac ccc gag gta gat gac cta	192			
Lys Ser Leu Arg Pro Asp Glu Leu Pro His Pro Glu Val Asp Asp Leu				
50 55 60				
gcc cag atc acc aca ttc tgg ggc cag	219			
Ala Gln Ile Thr Thr Phe Trp Gly Gln				
65 70				
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<222> (1)...(436)				
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1 5 10 15				
gag gtg agc gga aga act aat aaa gtg gtg gca aga ata gtg caa agc	96			
Glu Val Ser Gly Arg Thr Asn Lys Val Val Ala Arg Ile Val Gln Ser				
20 25 30				
cac cag cag act ggc cgt agc ggc tcc agg agg gag aaa gtg aga gag	144			
His Gln Gln Thr Gly Arg Ser Gly Ser Arg Arg Glu Lys Val Arg Glu				
35 40 45				
cgg agc cat cct aaa act ggg act gtg gat aat aac act tct aca gac	192			
Arg Ser His Pro Lys Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp				
50 55 60				
cta aaa tcc ctg aga cca gat gag cta ccg cac ccc gag gta gat gac	240			
Leu Lys Ser Leu Arg Pro Asp Glu Leu Pro His Pro Glu Val Asp Asp				
65 70 75 80				
cta gcc cag atc acc aca ttc tgg ggc cag tct cca caa acc gga gga	288			
Leu Ala Gln Ile Thr Thr Phe Trp Gly Gln Ser Pro Gln Thr Gly Gly				
85 90 95				
cta ccc cca gac tgc agt aag tgt tgt cat gga gac tac agc ttt cga	336			
Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Ser Phe Arg				
100 105 110				
ggc tac caa ggc ccc cct ggg cca ccg ggc cct cct ggc att cca gga	384			
Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly				
115 120 125				
aac cat gga aac aat ggc aac aat gga gcc act ggt cat gaa gga gcc	432			
Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu Gly Ala				
130 135 140				
aaa g	436			

Lys
145

<210> 6
<211> 391
<212> PRT
<213> Homo sapiens

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Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
35 40 45
Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
50 55 60
Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
65 70 75 80
Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
85 90 95
Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
100 105 110
Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
115 120 125
Asp Gly His Gln Met Ala Leu Asn Phe Phe Phe Pro Asp Glu Lys
130 135 140
Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145 150 155 160
Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
165 170 175
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
180 185 190
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
195 200 205
Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
210 215 220
Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225 230 235 240
Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
245 250 255
Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
260 265 270
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
275 280 285
Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
290 295 300
Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
305 310 315 320
Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
325 330 335
Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
340 345 350
Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
355 360 365
Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
370 375 380
Leu Gly Glu Ala Pro Ala Ser
385 390

<210> 7
<211> 957
<212> DNA
<213> Artificial Sequence

<220>
 <223> Degenerate polynucleotide sequence encoding a
 zacrp3x2 polypeptide of SEQ ID NO:2.

<221> misc_feature
 <222> (1)...(957)
 <223> n = A, T, C or G

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 gtncarwsnc aycarcacac nggnmgnwsn ggnwsnmgnm gngaraargt nmngngarmgn 180
 wsncayccna aracnggnac ngtngayaay aayacnwsna cngayytnaa rwsnytnmgn 240
 ccngaygary tncncaycc ngargtngay gayytngcnc arathacnac nttytggggg 300
 carwsnccnc aracngggng nytnccnccn gaytgywsna artgytgyca yggngaytay 360
 wsnttymgng gntaycargg nccnccnggn ccnccnggnc cncnccngnat hccnggnaay 420
 cayggnaaya ayggnaayaa yggngcnaacn ggncaygarg gngcnaargg ngaraarggn 480
 gayaarggng ayytnggncc nmngggngar mgnggncarc ayggncncaa rggngaraar 540
 ggntayccng gnathccncc ngarytnear athgcnttya tggcnwsnyt ngcnacncay 600
 ttywsnaayc araaywsngg nathathtty wsnwsngtng aracnaayat hggnaaytty 660
 ttygaygtna tgacnggnmg nttyggngcn ccngtnwsng gngtntaytt yttyacntty 720
 wsnatgatga arcaygarga ygtngargar gtntaygtnt ayytnatgca yaayggnaay 780
 acngtnttyw snatgtayws ntaygaratg aarggnaarw sngayacnws nwsnaaycay 840
 gcngtntyna arytngcnaa rggngaygar gtntggytnm gnatgggnaa yggngcnnytn 900
 cayggngayc aycarmgntt ywsnacntty gcnggntty tnytnntyga racnaar 957

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 <212> PRT
 <213> Artificial Sequence

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 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (7)...(7)
 <223> Each Xaa is asparagine or aspartic acid

<221> VARIANT
 <222> (8)...(11)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (12)...(12)
 <223> Xaa is phenylalanine, tyrosine, tryptophan or
 leucine

<221> VARIANT
 <222> (13)...(18)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (20)...(24)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (26)...(26)
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<221> VARIANT

<222> (28)...(28)
 <223> Xaa is any amino acid residue

<221> VARIANT
 <222> (30)...(30)
 <223> Xaa is any amino acid residue

<221> VARIANT
 <222> (31)...(31)
 <223> Xaa is phenyalanine or tyrosine

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 1 5 10 15
 Xaa Xaa Phe Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa
 20 25 30

<210> 9
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<210> 10
 <211> 23
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 <223> Oligonucleotide primer ZC21,196

<400> 10
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<210> 11
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<220>
 <223> Oligonucleotide primer ZC14,063

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<210> 12
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 <212> DNA
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 <223> Oligonucleotide primer ZC17,574

<400> 12
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<210> 13
 <211> 24
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC17,600

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 <210> 14
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 <212> DNA
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 <220>
 <223> Oligonucleotide primer ZC23,989

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 gccaaattga ccagtgccgt tccg 84

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 <220>
 <223> Oligonucleotide primer ZC23,899

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 <210> 16
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 <220>
 <223> Oligonucleotide primer ZC23,898

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 <210> 17
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 <223> Oligonucleotide primer ZC23,899

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 <210> 18
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 <223> Oligonucleotide primer ZC38,824

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 <211> 23
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<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38,825

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23

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<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC21,909

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<223> Oligonucleotide primer ZC20,838

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<223> Oligonucleotide primer ZC21,913

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tgaccagagg gattttat

18

<210> 23

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC21,914

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18